

#4



PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/868,123

DATE: 05/15/2002

TIME: 16:09:10

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Output Set: N:\CRF3\05152002\I868123.raw

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3 <110> APPLICANT: Collins, Mary
4     Donaldson, Debra
5     Fitz, Lora
6     Neben, Tamlyn
7     Whitters, Matthew
8     Wood, Clive
9     Wills-Karp, Marsha
10    Genetics Institute, Inc.
13 <120> TITLE OF INVENTION: Cytokine Receptor Chain
15 <130> FILE REFERENCE: GI 5268A
C--> 17 <140> CURRENT APPLICATION NUMBER: US/09/868,123
C--> 18 <141> CURRENT FILING DATE: 2002-04-02
20 <160> NUMBER OF SEQ ID NOS: 9
22 <170> SOFTWARE: PatentIn Ver. 2.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1525
26 <212> TYPE: DNA
27 <213> ORGANISM: Mus sp.
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (256)..(1404)
33 <400> SEQUENCE: 1
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36 ctacccttga acagtgcct ctctcaagac agtgctttgc tcttcacgta taaggaagga 120
38 aaacagtaga gattcaattt agtgtctaag gtggaaagga ggacaaagag gtcttgatgat 180
40 aactgcctgt gataatacat ttcttgagaa accatattat tgagtagagc tttcagcaca 240
42 ctaaatacctg gagaa atg gct ttt gtg cat atc aga tgc ttg tgt ttc att 291
43     Met Ala Phe Val His Ile Arg Cys Leu Cys Phe Ile
44         1             5             10
46 ctt ctt tgt aca ata act ggc tat tct ttg gag ata aaa gtt aat cct 339
47 Leu Leu Cys Thr Ile Thr Gly Tyr Ser Leu Glu Ile Lys Val Asn Pro
48         15             20             25
50 cct cag gat ttt gaa ata ttg gat cct gga tta ctt ggt tat ctc tat 387
51 Pro Gln Asp Phe Glu Ile Leu Asp Pro Gly Leu Leu Gly Tyr Leu Tyr
52         30             35             40
54 ttg caa tgg aaa cct cct gtg gtt ata gaa aaa ttt aag ggc tgt aca 435
55 Leu Gln Trp Lys Pro Pro Val Val Ile Glu Lys Phe Lys Gly Cys Thr
56 45             50             55             60
58 cta gaa tat gag tta aaa tac cga aat gtt gat agc gac agc tgg aag 483
59 Leu Glu Tyr Glu Leu Lys Tyr Arg Asn Val Asp Ser Asp Ser Trp Lys
60         65             70             75
62 act ata att act agg aat cta att tac aag gat ggg ttt gat ctt aat 531
63 Thr Ile Ile Thr Arg Asn Leu Ile Tyr Lys Asp Gly Phe Asp Leu Asn

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64		80		85		90		
66	aaa ggc att gaa gga aag ata cgt acg cat ttg tca gag cat tgt aca							579
67	Lys Gly Ile Glu Gly Lys Ile Arg Thr His Leu Ser Glu His Cys Thr							
68		95		100		105		
70	aat gga tca gaa gta caa agt cca tgg ata gaa gct tct tat ggg ata							627
71	Asn Gly Ser Glu Val Gln Ser Pro Trp Ile Glu Ala Ser Tyr Gly Ile							
72		110		115		120		
74	tca gat gaa gga agt ttg gaa act aaa att cag gac atg aag tgt ata							675
75	Ser Asp Glu Gly Ser Leu Glu Thr Lys Ile Gln Asp Met Lys Cys Ile							
76	125		130		135		140	
78	tat tat aac tgg cag tat ttg gtc tgc tct tgg aaa cct ggc aag aca							723
79	Tyr Tyr Asn Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Lys Thr							
80		145		150		155		
82	gta tat tct gat acc aac tat acc atg ttt ttc tgg tat gag ggc ttg							771
83	Val Tyr Ser Asp Thr Asn Tyr Thr Met Phe Phe Trp Tyr Glu Gly Leu							
84		160		165		170		
86	gat cat gcc tta cag tgt gct gat tac ctc cag cat gat gaa aaa aat							819
87	Asp His Ala Leu Gln Cys Ala Asp Tyr Leu Gln His Asp Glu Lys Asn							
88		175		180		185		
90	gtt gga tgc aaa ctg tcc aac ttg gac tca tca gac tat aaa gat ttt							867
91	Val Gly Cys Lys Leu Ser Asn Leu Asp Ser Ser Asp Tyr Lys Asp Phe							
92		190		195		200		
94	ttt atc tgt gtt aat gga tct tca aag ttg gaa ccc atc aga tcc agc							915
95	Phe Ile Cys Val Asn Gly Ser Ser Lys Leu Glu Pro Ile Arg Ser Ser							
96	205		210		215		220	
98	tat aca gtt ttt caa ctt caa aat ata gtt aaa cca ttg cca cca gaa							963
99	Tyr Thr Val Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Glu							
100		225		230		235		
102	ttc ctt cat att agt gtg gag aat tcc att gat att aga atg aaa tgg							1011
103	Phe Leu His Ile Ser Val Glu Asn Ser Ile Asp Ile Arg Met Lys Trp							
104		240		245		250		
106	agc aca cct gga gga ccc att cca cca agg tgt tac act tat gaa att							1059
107	Ser Thr Pro Gly Gly Pro Ile Pro Pro Arg Cys Tyr Thr Tyr Glu Ile							
108		255		260		265		
110	gtg atc cga gaa gac gat att tcc tgg gag tct gcc aca gac aaa aac							1107
111	Val Ile Arg Glu Asp Asp Ile Ser Trp Glu Ser Ala Thr Asp Lys Asn							
112		270		275		280		
114	gat atg aag ttg aag agg aga gca aat gaa agt gaa gac cta tgc ttt							1155
115	Asp Met Lys Leu Lys Arg Ala Asn Glu Ser Glu Asp Leu Cys Phe							
116	285		290		295		300	
118	ttt gta aga tgt aag gtc aat ata tat tgt gca gat gat gga att tgg							1203
119	Phe Val Arg Cys Lys Val Asn Ile Tyr Cys Ala Asp Asp Gly Ile Trp							
120		305		310		315		
122	agc gaa tgg agt gaa gag gaa tgt tgg gaa ggt tac aca ggg cca gac							1251
123	Ser Glu Trp Ser Glu Glu Glu Cys Trp Glu Gly Tyr Thr Gly Pro Asp							
124		320		325		330		
126	tca aag att att ttc ata gta cca gtt tgt ctt ttc ttt ata ttc ctt							1299
127	Ser Lys Ile Ile Phe Ile Val Pro Val Cys Leu Phe Phe Ile Phe Leu							
128		335		340		345		

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130 ttg tta ctt ctt tgc ctt att gtg gag aag gaa gaa cct gaa ccc aca 1347
131 Leu Leu Leu Leu Cys Leu Ile Val Glu Lys Glu Glu Pro Glu Pro Thr
132 350 355 360
134 ttg agc ctc cat gtg gat ctg aac aaa gaa gtg tgt gct tat gaa gat 1395
135 Leu Ser Leu His Val Asp Leu Asn Lys Glu Val Cys Ala Tyr Glu Asp
136 365 370 375 380
138 acc ctc tgt taaaccacca atttcttgac atagagccag ccagcaggag 1444
139 Thr Leu Cys
141 tcatattaaa ctcaatttct cttaaaattt cgaatacatc ttcttgaaaa tccaaaaaaa 1504
143 aaaaaaaaaa aaaaactcga g 1525
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147 <211> LENGTH: 383
148 <212> TYPE: PRT
149 <213> ORGANISM: Mus sp.
151 <400> SEQUENCE: 2
152 Met Ala Phe Val His Ile Arg Cys Leu Cys Phe Ile Leu Leu Cys Thr
153 1 5 10 15
155 Ile Thr Gly Tyr Ser Leu Glu Ile Lys Val Asn Pro Pro Gln Asp Phe
156 20 25 30
158 Glu Ile Leu Asp Pro Gly Leu Leu Gly Tyr Leu Tyr Leu Gln Trp Lys
159 35 40 45
161 Pro Pro Val Val Ile Glu Lys Phe Lys Gly Cys Thr Leu Glu Tyr Glu
162 50 55 60
164 Leu Lys Tyr Arg Asn Val Asp Ser Asp Ser Trp Lys Thr Ile Ile Thr
165 65 70 75 80
167 Arg Asn Leu Ile Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile Glu
168 85 90 95
170 Gly Lys Ile Arg Thr His Leu Ser Glu His Cys Thr Asn Gly Ser Glu
171 100 105 110
173 Val Gln Ser Pro Trp Ile Glu Ala Ser Tyr Gly Ile Ser Asp Glu Gly
174 115 120 125
176 Ser Leu Glu Thr Lys Ile Gln Asp Met Lys Cys Ile Tyr Tyr Asn Trp
177 130 135 140
179 Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Lys Thr Val Tyr Ser Asp
180 145 150 155 160
182 Thr Asn Tyr Thr Met Phe Phe Trp Tyr Glu Gly Leu Asp His Ala Leu
183 165 170 175
185 Gln Cys Ala Asp Tyr Leu Gln His Asp Glu Lys Asn Val Gly Cys Lys
186 180 185 190
188 Leu Ser Asn Leu Asp Ser Ser Asp Tyr Lys Asp Phe Phe Ile Cys Val
189 195 200 205
191 Asn Gly Ser Ser Lys Leu Glu Pro Ile Arg Ser Ser Tyr Thr Val Phe
192 210 215 220
194 Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Glu Phe Leu His Ile
195 225 230 235 240
197 Ser Val Glu Asn Ser Ile Asp Ile Arg Met Lys Trp Ser Thr Pro Gly
198 245 250 255
200 Gly Pro Ile Pro Pro Arg Cys Tyr Thr Tyr Glu Ile Val Ile Arg Glu
201 260 265 270

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203 Asp Asp Ile Ser Trp Glu Ser Ala Thr Asp Lys Asn Asp Met Lys Leu
204      275      280      285
206 Lys Arg Arg Ala Asn Glu Ser Glu Asp Leu Cys Phe Phe Val Arg Cys
207      290      295      300
209 Lys Val Asn Ile Tyr Cys Ala Asp Asp Gly Ile Trp Ser Glu Trp Ser
210 305      310      315      320
212 Glu Glu Glu Cys Trp Glu Gly Tyr Thr Gly Pro Asp Ser Lys Ile Ile
213      325      330      335
215 Phe Ile Val Pro Val Cys Leu Phe Phe Ile Phe Leu Leu Leu Leu Leu
216      340      345      350
218 Cys Leu Ile Val Glu Lys Glu Glu Pro Glu Pro Thr Leu Ser Leu His
219      355      360      365
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222      370      375      380
225 <210> SEQ ID NO: 3
226 <211> LENGTH: 1369
227 <212> TYPE: DNA
228 <213> ORGANISM: Homo sapiens
230 <220> FEATURE:
231 <221> NAME/KEY: CDS
232 <222> LOCATION: (103)..(1245)
234 <400> SEQUENCE: 3
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237 ggcgggggaga gaggcaatat caaggtttta aatctcggag aa atg gct ttc gtt 114
238      Met Ala Phe Val
239      1
241 tgc ttg gct atc gga tgc tta tat acc ttt ctg ata agc aca aca ttt 162
242 Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile Ser Thr Thr Phe
243 5      10      15      20
245 ggc tgt act tca tct tca gac acc gag ata aaa gtt aac cct cct cag 210
246 Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val Asn Pro Pro Gln
247      25      30      35
249 gat ttt gag ata gtg gat ccc gga tac tta ggt tat ctc tat ttg caa 258
250 Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Tyr Leu Gln
251      40      45      50
253 tgg caa ccc cca ctg tct ctg gat cat ttt aag gaa tgc aca gtg gaa 306
254 Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu Cys Thr Val Glu
255      55      60      65
257 tat gaa cta aaa tac cga aac att ggt agt gaa aca tgg aag acc atc 354
258 Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr Trp Lys Thr Ile
259      70      75      80
261 att act aag aat cta cat tac aaa gat ggg ttt gat ctt aac aag ggc 402
262 Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly
263 85      90      95      100
265 att gaa gcg aag ata cac acg ctt tta cca tgg caa tgc aca aat gga 450
266 Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln Cys Thr Asn Gly
267      105      110      115
269 tca gaa gtt caa agt tcc tgg gca gaa act act tat tgg ata tca cca 498
270 Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr Trp Ile Ser Pro

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271					120				125				130				
273	caa	gga	att	cca	gaa	act	aaa	gtt	cag	gat	atg	gat	tgc	gta	tat	tac	546
274	Gln	Gly	Ile	Pro	Glu	Thr	Lys	Val	Gln	Asp	Met	Asp	Cys	Val	Tyr	Tyr	.
275	135				140				145								
277	aat	tgg	caa	tat	tta	ctc	tgt	tct	tgg	aaa	cct	ggc	ata	ggg	gta	ctt	594
278	Asn	Trp	Gln	Tyr	Leu	Leu	Cys	Ser	Trp	Lys	Pro	Gly	Ile	Gly	Val	Leu	
279	150				155				160								
281	ctt	gat	acc	aat	tac	aac	ttg	ttt	tac	tgg	tat	gag	ggc	ttg	gat	cat	642
282	Leu	Asp	Thr	Asn	Tyr	Asn	Leu	Phe	Tyr	Trp	Tyr	Glu	Gly	Leu	Asp	His	
283	165				170				175				180				
285	gca	tta	cag	tgt	gtt	gat	tac	atc	aag	gct	gat	gga	caa	aat	ata	gga	690
286	Ala	Leu	Gln	Cys	Val	Asp	Tyr	Ile	Lys	Ala	Asp	Gly	Gln	Asn	Ile	Gly	
287	185				190				195								
289	tgc	aga	ttt	ccc	tat	ttg	gag	gca	tca	gac	tat	aaa	gat	ttc	tat	att	738
290	Cys	Arg	Phe	Pro	Tyr	Leu	Glu	Ala	Ser	Asp	Tyr	Lys	Asp	Phe	Tyr	Ile	
291	200				205				210								
293	tgt	gtt	aat	gga	tca	tca	gag	aac	aag	cct	atc	aga	toc	agt	tat	ttc	786
294	Cys	Val	Asn	Gly	Ser	Ser	Glu	Asn	Lys	Pro	Ile	Arg	Ser	Ser	Tyr	Phe	
295	215				220				225								
297	act	ttt	cag	ctt	caa	aat	ata	gtt	aaa	cct	ttg	ccg	cca	gtc	tat	ctt	834
298	Thr	Phe	Gln	Leu	Gln	Asn	Ile	Val	Lys	Pro	Leu	Pro	Pro	Val	Tyr	Leu	
299	230				235				240								
301	act	ttt	act	cgg	gag	agt	tca	tgt	gaa	att	aag	ctg	aaa	tgg	agc	ata	882
302	Thr	Phe	Thr	Arg	Glu	Ser	Ser	Cys	Glu	Ile	Lys	Leu	Lys	Trp	Ser	Ile	
303	245				250				255				260				
305	cct	ttg	gga	cct	att	cca	gca	agg	tgt	ttt	gat	tat	gaa	att	gag	atc	930
306	Pro	Leu	Gly	Pro	Ile	Pro	Ala	Arg	Cys	Phe	Asp	Tyr	Glu	Ile	Glu	Ile	
307	265				270				275								
309	aga	gaa	gat	gat	act	acc	ttg	gtg	act	gct	aca	gtt	gaa	aat	gaa	aca	978
310	Arg	Glu	Asp	Asp	Thr	Thr	Leu	Val	Thr	Ala	Thr	Val	Glu	Asn	Glu	Thr	
311	280				285				290								
313	tac	acc	ttg	aaa	aca	aca	aat	gaa	acc	cga	caa	tta	tgc	ttt	gta	gta	1026
314	Tyr	Thr	Leu	Lys	Thr	Thr	Asn	Glu	Thr	Arg	Gln	Leu	Cys	Phe	Val	Val	
315	295				300				305								
317	aga	agc	aaa	gtg	aat	att	tat	tgc	tca	gat	gac	gga	att	tgg	agt	gag	1074
318	Arg	Ser	Lys	Val	Asn	Ile	Tyr	Cys	Ser	Asp	Asp	Gly	Ile	Trp	Ser	Glu	
319	310				315				320								
321	tgg	agt	gat	aaa	caa	tgc	tgg	gaa	ggg	gaa	gac	cta	tcg	aag	aaa	act	1122
322	Trp	Ser	Asp	Lys	Gln	Cys	Trp	Glu	Gly	Glu	Asp	Leu	Ser	Lys	Lys	Thr	
323	325				330				335				340				
325	ttg	cta	cgt	ttc	tgg	cta	cca	ttt	ggg	ttc	atc	tta	ata	tta	gtt	ata	1170
326	Leu	Leu	Arg	Phe	Trp	Leu	Pro	Phe	Gly	Phe	Ile						

VERIFICATION SUMMARY

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L:17 M:270 C: Current Application Number differs, Replaced Current Application Number

L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date